

0570
08/4

CRF Errors Corrected by the STIC Systems Branch

#2

Serial Number: 09/920033

CRF Processing Date: 10/05/01
Edited by: mt
Verified by: _____ (ST)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data"
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/920,033

DATE: 10/05/2001

TIME: 13:13:52

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10052001\I920033.raw

ENTERED

6 <110> APPLICANT: Rosanne M. Crooke
 7 Mark J. Graham
 10 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
 12 <130> FILE REFERENCE: ISPH-0592
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/920,033
 C--> 14 <141> CURRENT FILING DATE: 2001-08-01
 14 <160> NUMBER OF SEQ ID NOS: 123
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 20
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Antisense Oligonucleotide
 24 <400> SEQUENCE: 1
 25 tccgtcatcg ctccctcaggg 20
 27 <210> SEQ ID NO: 2
 28 <211> LENGTH: 20
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Artificial Sequence
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: Antisense Oligonucleotide
 35 <400> SEQUENCE: 2
 36 atgcattctg cccccaagga 20
 38 <210> SEQ ID NO: 3
 39 <211> LENGTH: 14121
 40 <212> TYPE: DNA
 41 <213> ORGANISM: Homo sapiens
 43 <220> FEATURE:
 44 <221> NAME/KEY: CDS
 45 <222> LOCATION: (129)...(13820)
 47 <400> SEQUENCE: 3
 48 attcccaccg ggacctgcgg ggetgagtgc ccttctcggt tgetgccgct gaggagcccg 60
 49 cccagccagc cagggccgcg aggccgaggc cagggccgag cccaggagcc gccccaccgc 120
 50 agctggcg atg gac ccg ccg agg ccc gcg ctg ctg gcg ctg ctg gcg ctg 170
 51 Met Asp Pro Pro Arg Pro Ala Leu Leu Ala Leu Leu Ala Leu
 52 1 5 10
 54 cct gcg ctg ctg ctg ctg ctg gcg ggc gcc agg gcc gaa gag gaa 218
 55 Pro Ala Leu Leu Leu Leu Leu Ala Gly Ala Arg Ala Glu Glu Glu
 56 15 20 25 30
 58 atg ctg gaa aat gtc agc ctg gtc tgt cca aaa gat gcg acc cga ttc 266
 59 Met Leu Glu Asn Val Ser Leu Val Cys Pro Lys Asp Ala Thr Arg Phe
 60 35 40 45
 62 aag cac ctc cgg aag tac aca tac aac tat gag gct gag agt tcc agt 314
 63 Lys His Leu Arg Lys Tyr Thr Tyr Asn Tyr Glu Ala Glu Ser Ser Ser
 64 50 55 60
 66 gga gtc cct ggg act gct gat tca aga agt gcc acc agg atc aac tgc 362
 67 Gly Val Pro Gly Thr Ala Asp Ser Arg Ser Ala Thr Arg Ile Asn Cys

Non Entered

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Input Set : A:\PTO.MH.txt

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68	65	70	75	
70	aag gtt gag ctg gag gtt ccc cag ctc tgc agc ttc atc ctg aag acc	410		
71	Lys Val Glu Leu Glu Val Pro Gln Leu Cys Ser Phe Ile Leu Lys Thr			
72	80	85	90	
74	agc cag tgc acc ctg aaa gag gtg tat ggc ttc aac cct gag ggc aaa	458		
75	Ser Gln Cys Thr Leu Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys			
76	95	100	105	110
78	gcc ttg ctg aag aaa acc aag aac tct gag gag ttt gct gca gcc atg	506		
79	Ala Leu Leu Lys Thr Lys Asn Ser Glu Glu Phe Ala Ala Ala Met			
80	115	120	125	
82	tcc agg tat gag ctc aag ctg gcc att cca gaa ggg aag cag gtt ttc	554		
83	Ser Arg Tyr Glu Leu Lys Leu Ala Ile Pro Glu Gly Lys Gln Val Phe			
84	130	135	140	
86	ctt tac ccg gag aaa gat gaa cct act tac atc ctg aac atc aag agg	602		
87	Leu Tyr Pro Glu Lys Asp Glu Pro Thr Tyr Ile Leu Asn Ile Lys Arg			
88	145	150	155	
90	ggc atc att tct gcc ctc ctg gtt ccc cca gag aca gaa gaa gcc aag	650		
91	Gly Ile Ile Ser Ala Leu Leu Val Pro Pro Glu Thr Glu Glu Ala Lys			
92	160	165	170	
94	caa gtg ttg ttt ctg gat acc gtg tat gga aac tgc tcc act cac ttt	698		
95	Gln Val Leu Phe Leu Asp Thr Val Tyr Gly Asn Cys Ser Thr His Phe			
96	175	180	185	190
98	acc gtc aag acg agg aag ggc aat gtg gca aca gaa ata tcc act gaa	746		
99	Thr Val Lys Thr Arg Lys Gly Asn Val Ala Thr Glu Ile Ser Thr Glu			
100	195	200	205	
102	aga gac ctg ggg cag tgt gat cgc ttc aag ccc atc cgc aca ggc atc	794		
103	Arg Asp Leu Gly Gln Cys Asp Arg Phe Lys Pro Ile Arg Thr Gly Ile			
104	210	215	220	
106	agc cca ctt gct ctc atc aaa ggc atg acc cgc ccc ttg tca act ctg	842		
107	Ser Pro Leu Ala Leu Ile Lys Gly Met Thr Arg Pro Leu Ser Thr Leu			
108	225	230	235	
110	atc agc agc agc cag tcc tgt cag tac aca ctg gac gct aag agg aag	890		
111	Ile Ser Ser Ser Gln Ser Cys Gln Tyr Thr Leu Asp Ala Lys Arg Lys			
112	240	245	250	
114	cat gtg gca gaa gcc atc tgc aag gag caa cac ctc ttc ctg cct ttc	938		
115	His Val Ala Glu Ala Ile Cys Lys Glu Gln His Leu Phe Leu Pro Phe			
116	255	260	265	270
118	tcc tac aac aat aag tat ggg atg gta gca caa gtg aca cag act ttg	986		
119	Ser Tyr Asn Asn Lys Tyr Gly Met Val Ala Gln Val Thr Gln Thr Leu			
120	275	280	285	
122	aaa ctt gaa gac aca cca aag atc aac agc cgc ttc ttt ggt gaa ggt	1034		
123	Lys Leu Glu Asp Thr Pro Lys Ile Asn Ser Arg Phe Phe Gly Glu Gly			
124	290	295	300	
126	act aag aag atg ggc ctc gca ttt gag agc acc aaa tcc aca tca cct	1082		
127	Thr Lys Lys Met Gly Leu Ala Phe Glu Ser Thr Lys Ser Thr Ser Pro			
128	305	310	315	
130	cca aag cag gcc gaa gct gtt ttg aag act ctc cag gaa ctg aaa aaa	1130		
131	Pro Lys Gln Ala Glu Ala Val Leu Lys Thr Leu Gln Glu Leu Lys Lys			
132	320	325	330	

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134 cta acc atc tct gag caa aat atc cag aga gct aat ctc ttc aat aag 1178
135 Leu Thr Ile Ser Glu Gln Asn Ile Gln Arg Ala Asn Leu Phe Asn Lys
136 335 340 345 350
138 ctg gtt act gag ctg aga ggc ctc agt gat gaa gca gtc aca tct ctc 1226
139 Leu Val Thr Glu Leu Arg Gly Leu Ser Asp Glu Ala Val Thr Ser Leu
140 355 360 365
142 ttg cca cag ctg att gag gtg tcc agc ccc atc act tta caa gcc ttg 1274
143 Leu Pro Gln Leu Ile Glu Val Ser Ser Pro Ile Thr Leu Gln Ala Leu
144 370 375 380
146 gtt cag tgt gga cag cct cag tgc tcc act cac atc ctc cag tgg ctg 1322
147 Val Gln Cys Gly Gln Pro Gln Cys Ser Thr His Ile Leu Gln Trp Leu
148 385 390 395
150 aaa cgt gtg cat gcc aac ccc ctt ctg ata gat gtg gtc acc tac ctg 1370
151 Lys Arg Val His Ala Asn Pro Leu Leu Ile Asp Val Val Thr Tyr Leu
152 400 405 410
154 gtg gcc ctg atc ccc gag ccc tca gca cag cag ctg cga gag atc ttc 1418
155 Val Ala Leu Ile Pro Glu Pro Ser Ala Gln Gln Leu Arg Glu Ile Phe
156 415 420 425 430
158 aac atg gcg agg gat cag cgc agc cga gcc acc ttg tat gcg ctg agc 1466
159 Asn Met Ala Arg Asp Gln Arg Ser Arg Ala Thr Leu Tyr Ala Leu Ser
160 435 440 445
162 cac gcg gtc aac aac tat cat aag aca aac cct aca ggg acc cag gag 1514
163 His Ala Val Asn Asn Tyr His Lys Thr Asn Pro Thr Gly Thr Gln Glu
164 450 455 460
166 ctg ctg gac att gct aat tac ctg atg gaa cag att caa gat gac tgc 1562
167 Leu Leu Asp Ile Ala Asn Tyr Leu Met Glu Gln Ile Gln Asp Asp Cys
168 465 470 475
170 act ggg gat gaa gat tac acc tat ttg att ctg cgg gtc att gga aat 1610
171 Thr Gly Asp Glu Asp Tyr Thr Tyr Leu Ile Leu Arg Val Ile Gly Asn
172 480 485 490
174 atg ggc caa acc atg gag cag tta act cca gaa ctc aag tct tca atc 1658
175 Met Gly Gln Thr Met Glu Gln Leu Thr Pro Glu Leu Lys Ser Ser Ile
176 495 500 505 510
178 ctc aaa tgt gtc caa agt aca aag cca tca ctg atg atc cag aaa gct 1706
179 Leu Lys Cys Val Gln Ser Thr Lys Pro Ser Leu Met Ile Gln Lys Ala
180 515 520 525
182 gcc atc cag gct ctg cgg aaa atg gag cct aaa gac aag gac cag gag 1754
183 Ala Ile Gln Ala Leu Arg Lys Met Glu Pro Lys Asp Lys Asp Gln Glu
184 530 535 540
186 gtt ctt ctt cag act ttc ctt gat gat gct tct ccg gga gat aag cga 1802
187 Val Leu Leu Gln Thr Phe Leu Asp Ala Ser Pro Gly Asp Lys Arg
188 545 550 555
190 ctg gct gcc tat ctt atg ttg atg agg agt cct tca cag gca gat att 1850
191 Leu Ala Ala Tyr Leu Met Leu Met Arg Ser Pro Ser Gln Ala Asp Ile
192 560 565 570
194 aac aaa att gtc caa att cta cca tgg gaa cag aat gag caa gtg aag 1898
195 Asn Lys Ile Val Gln Ile Leu Pro Trp Glu Gln Asn Glu Gln Val Lys
196 575 580 585 590
198 aac ttt gtg gct tcc cat att gcc aat atc ttg aac tca gaa gaa ttg 1946

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199 Asn Phe Val Ala Ser His Ile Ala Asn Ile Leu Asn Ser Glu Glu Leu
200          595          600          605
202 gat atc caa gat ctg aaa aag tta gtg aaa gaa gct ctg aaa gaa tct 1994
203 Asp Ile Gln Asp Leu Lys Lys Leu Val Lys Glu Ala Leu Lys Glu Ser
204          610          615          620
206 caa ctt cca act gtc atg gac ttc aga aaa ttc tct cgg aac tat caa 2042
207 Gln Leu Pro Thr Val Met Asp Phe Arg Lys Phe Ser Arg Asn Tyr Gln
208          625          630          635
210 ctc tac aaa tct gtt tct ctt cca tca ctt gac cca gcc tca gcc aaa 2090
211 Leu Tyr Lys Ser Val Ser Leu Pro Ser Leu Asp Pro Ala Ser Ala Lys
212          640          645          650
214 ata gaa ggg aat ctt ata ttt gat cca aat aac tac ctt cct aaa gaa 2138
215 Ile Glu Gly Asn Leu Ile Phe Asp Pro Asn Asn Tyr Leu Pro Lys Glu
216 655          660          665          670
218 agc atg ctg aaa act acc ctc act gcc ttt gga ttt gct tca gct gac 2186
219 Ser Met Leu Lys Thr Thr Leu Thr Ala Phe Gly Phe Ala Ser Ala Asp
220          675          680          685
222 ctc atc gag att ggc ttg gaa gga aaa ggc ttt gag cca aca ttg gaa 2234
223 Leu Ile Glu Ile Gly Leu Glu Gly Lys Gly Phe Glu Pro Thr Leu Glu
224          690          695          700
226 gct ctt ttt ggg aag caa gga ttt ttc cca gac agt gtc aac aaa gct 2282
227 Ala Leu Phe Gly Lys Gln Gly Phe Phe Pro Asp Ser Val Asn Lys Ala
228          705          710          715
230 ttg tac tgg gtt aat ggt caa gtt cct gat ggt gtc tct aag gtc tta 2330
231 Leu Tyr Trp Val Asn Gly Gln Val Pro Asp Gly Val Ser Lys Val Leu
232          720          725          730
234 gtg gac cac ttt ggc tat acc aaa gat gat aaa cat gag cag gat atg 2378
235 Val Asp His Phe Gly Tyr Thr Lys Asp Asp Lys His Glu Gln Asp Met
236 735          740          745          750
238 gta aat gga ata atg ctc agt gtt gag aag ctg att aaa gat ttg aaa 2426
239 Val Asn Gly Ile Met Leu Ser Val Glu Lys Leu Ile Lys Asp Leu Lys
240          755          760          765
242 tcc aaa gaa gtc ccg gaa gcc aga gcc tac ctc cgc atc ttg gga gag 2474
243 Ser Lys Glu Val Pro Glu Ala Arg Ala Tyr Leu Arg Ile Leu Gly Glu
244          770          775          780
246 gag ctt ggt ttt gcc agt ctc cat gac ctc cag ctc ctg gga aag ctg 2522
247 Glu Leu Gly Phe Ala Ser Leu His Asp Leu Gln Leu Leu Gly Lys Leu
248          785          790          795
250 ctt ctg atg ggt gcc cgc act ctg cag ggg atc ccc cag atg att gga 2570
251 Leu Leu Met Gly Ala Arg Thr Leu Gln Gly Ile Pro Gln Met Ile Gly
252          800          805          810
254 gag gtc atc agg aag ggc tca aag aat gac ttt ttt ctt cac tac atc 2618
255 Glu Val Ile Arg Lys Gly Ser Lys Asn Asp Phe Phe Leu His Tyr Ile
256 815          820          825          830
258 ttc atg gag aat gcc ttt gaa ctc ccc act gga gct gga tta cag ttg 2666
259 Phe Met Glu Asn Ala Phe Glu Leu Pro Thr Gly Ala Gly Leu Gln Leu
260          835          840          845
262 caa ata tct tca tct gga gtc att gct ccc gga gcc aag gct gga gta 2714
263 Gln Ile Ser Ser Ser Gly Val Ile Ala Pro Gly Ala Lys Ala Gly Val

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264		850		855		860		
266	aaa	ctg	gaa	gta	gcc	aac	atg	cag
267	Lys	Leu	Glu	Val	Ala	Asn	Met	Gln
268			865			870		875
270	gtg	tct	gtg	gag	ttt	gtg	aca	aat
271	Val	Ser	Val	Glu	Phe	Val	Thr	Asn
272		880				885		890
274	gct	agg	agt	ggg	gtc	cag	atg	aac
275	Ala	Arg	Ser	Gly	Val	Gln	Met	Asn
276	895				900			905
278	ctg	gag	gct	cat	gtt	gcc	cta	aaa
279	Leu	Glu	Ala	His	Val	Ala	Leu	Lys
280				915				920
282	cct	tcc	cca	aag	aga	cca	gtc	aag
283	Pro	Ser	Pro	Lys	Arg	Pro	Val	Lys
284			930					935
286	cat	ttg	gtc	tct	acc	acc	aaa	acg
287	His	Leu	Val	Ser	Thr	Thr	Lys	Thr
288			945					950
290	aac	agg	cag	tcc	tgg	tca	gtt	tgc
291	Asn	Arg	Gln	Ser	Trp	Ser	Val	Cys
292		960				965		970
294	tac	tgc	acc	tca	ggc	gct	tac	tcc
295	Tyr	Cys	Thr	Ser	Gly	Ala	Tyr	Ser
296	975				980			985
298	tcc	tac	tat	ccg	ctg	acc	ggg	gac
299	Ser	Tyr	Tyr	Pro	Leu	Thr	Gly	Asp
300				995				1000
302	cct	aca	gga	gag	att	gag	cag	tat
303	Pro	Thr	Gly	Glu	Ile	Glu	Gln	Tyr
304			1010					1015
306	cag	aga	gag	gac	aga	gcc	ttg	gtg
307	Gln	Arg	Glu	Asp	Arg	Ala	Leu	Val
308		1025				1030		1035
310	gca	gaa	ggt	gcg	aag	cag	act	gag
311	Ala	Glu	Gly	Ala	Lys	Gln	Thr	Glu
312		1040				1045		1050
314	cgg	cag	agt	atg	acc	ttg	tcc	agt
315	Arg	Gln	Ser	Met	Thr	Leu	Ser	Ser
316	1055				1060			1065
318	gtt	gac	ctc	gga	aca	atc	ctc	aga
319	Val	Asp	Leu	Gly	Thr	Ile	Leu	Arg
320			1075					1080
322	aaa	acg	tct	tac	aga	ctc	acc	ctg
323	Lys	Thr	Ser	Tyr	Arg	Leu	Thr	Leu
324			1090					1095
326	gag	gtc	gcc	ctc	atg	ggc	cac	cta
327	Glu	Val	Ala	Leu	Met	Gly	His	Leu
328		1105						1110

VERIFICATION SUMMARY

DATE: 10/05/2001

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Input Set : A:\PTO.MH.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date